English translation of annex to IPER

CLAIMS

1. HIV gp120 mutants characterized in that they contain in their α2 structure or in both α2 and α1 structures, a mutation of one or more aromatic amino acids, and in that this mutation gives rise to a loss in the infective properties of the mutants relative to wild gp120.

2. Mutants according to claim 1, characterized in that the muted amino acid or acids are positioned in the gp120 region corresponding to the interaction cavity with CD4, such as identified by crystallography.

3. Mutants according to claim 2, in which W at position 112 is replaced by a non-aromatic amino acid.

4. Mutants according to claim 3, characterized in that the non-aromatic amino acid is chosen from among a serine or an isoleucine.

5. Mutants according to any of claims 2 to 4, characterized in that they contain an additional mutation according to which F at position 383 is replaced by an alanine.

6. Mutants according to claim 5, characterized by a mutation of tryptophan at position 427 to glycine, and/or of tryptophan at position 479 to serine.

7. Mutants according to claim 1, characterized in that they contain at least one mutation which is located in the gp120 region corresponding to the α2 helical structure, downstream from the V3 loop of gp120.

8. Mutants according to claim 7, characterized in that W at position 338 is replaced by a non-aromatic amino acid.

9. Mutants according to claim 8, characterized in that the non-aromatic amino acid is chosen from among a serine or an isoleucine.

10. Application of the mutants according to any of claims 1 to 9, as vaccine targets.

11. Application according to claim 10, characterized in that as antigenic vaccine target, a mutant is used in which W at position 338 is replaced by a non-aromatic amino acid.

12. Application according to claim 10, characterized in that the non-aromatic amino acid is chosen from among a serine or an isoleucine.

13. Method for suppressing the infectivity of an HIV gp120, characterized in that the α2 structure, or both the α2 and α1 structures, are muted on one or more aromatic amino acids.

14. Method according to claim 13, characterized in that mutation in the α1 structure is conducted in the gp120 region corresponding to the interaction cavity with CD4, such as identified by crystallography.